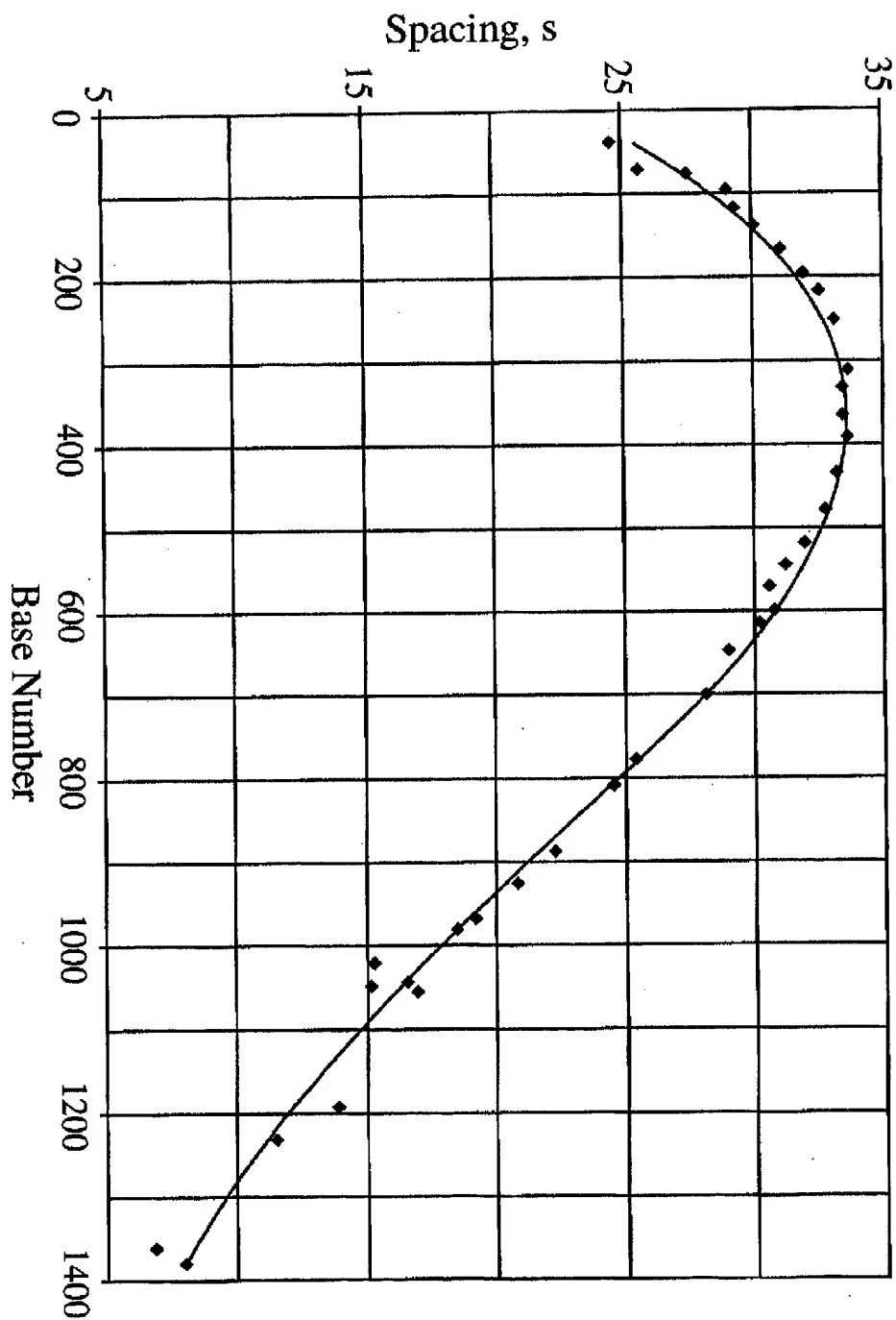


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Spacing Between Adjacent Peaks in the Raw Data  
(M13, T's T=6% 60C, Long Gel)

**FIG. 1**

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Spacing Between Adjacent Bases  
(for Different Number of Peaks Used for Alignment of Raw Data  
(M13, Long Gel, 55C, T=6%))

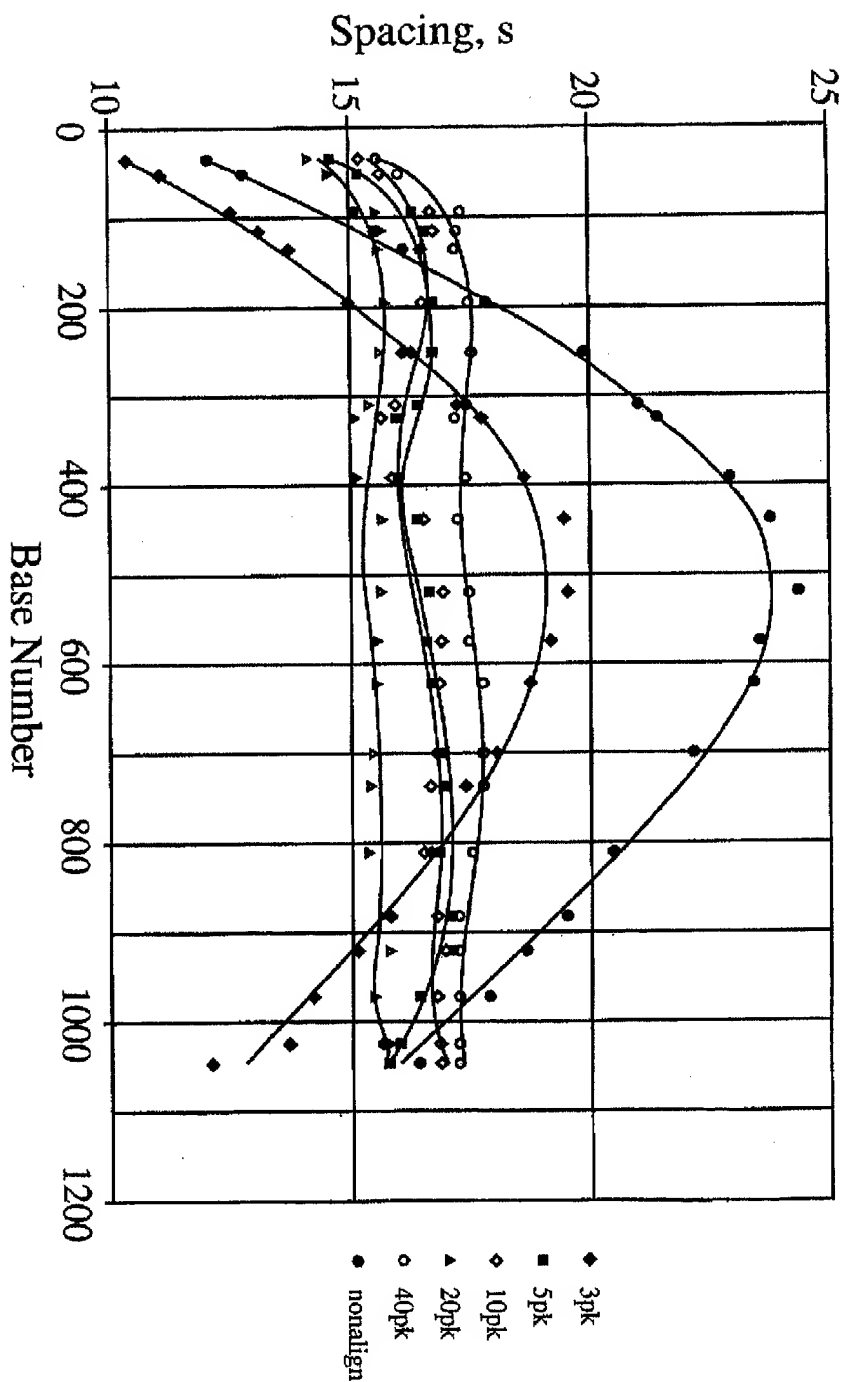
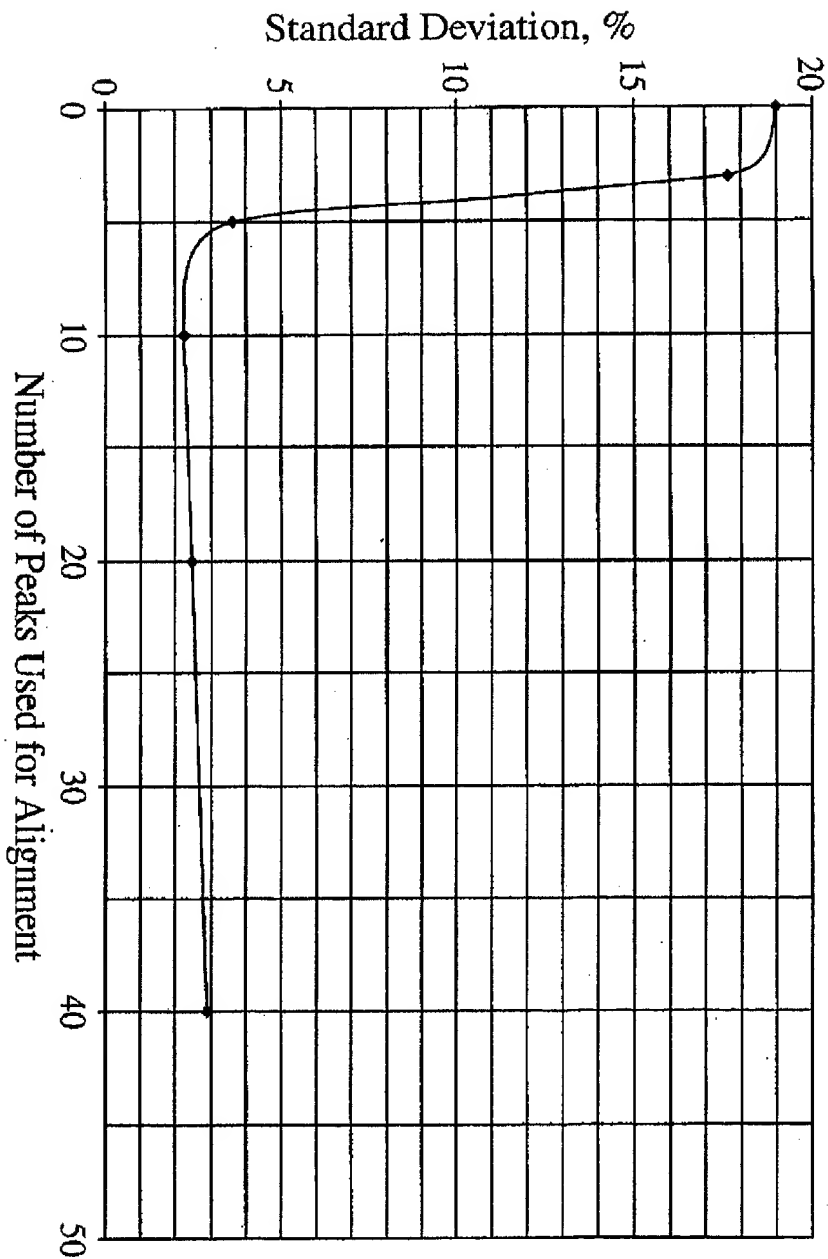
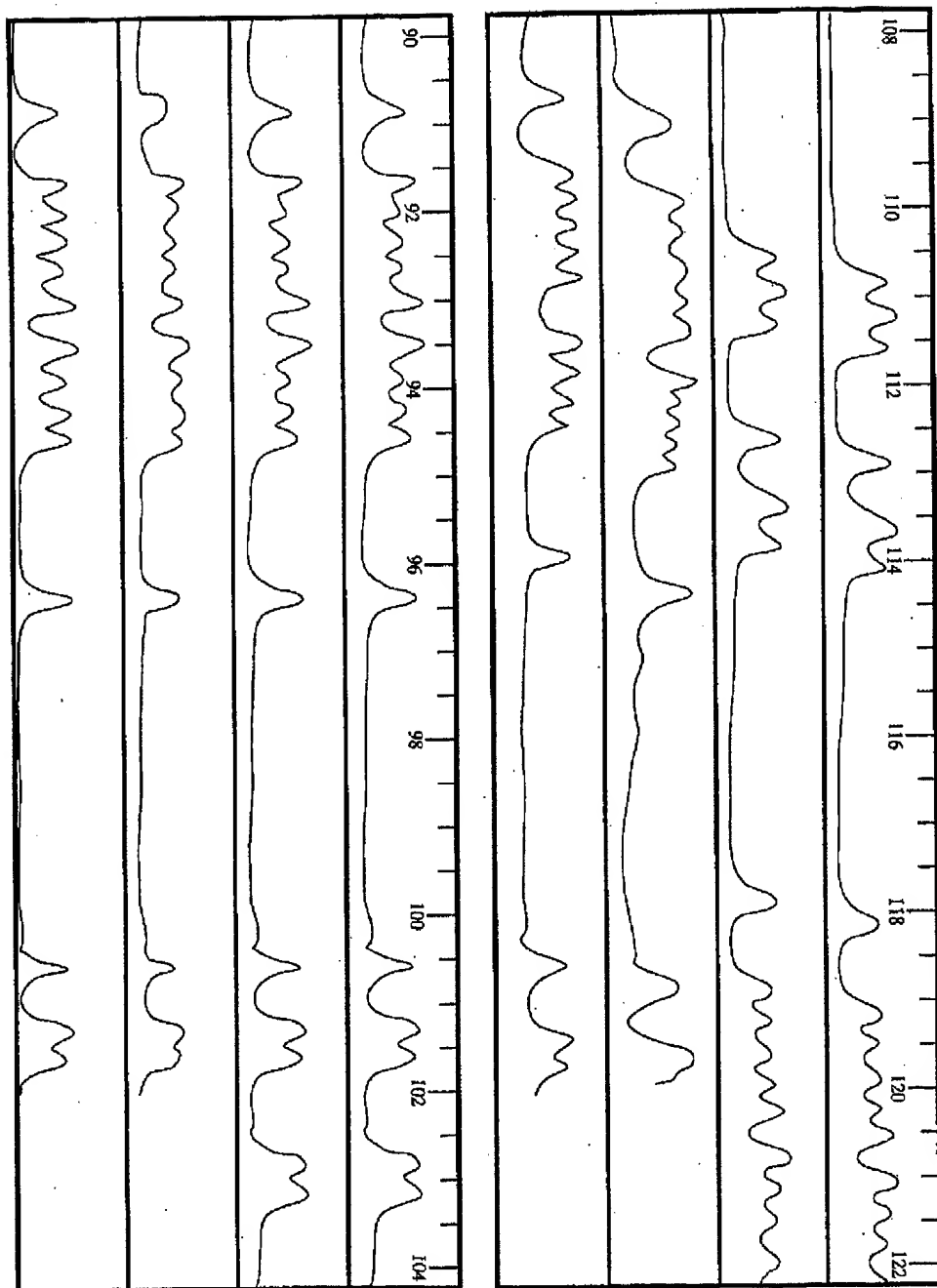


FIG. 2

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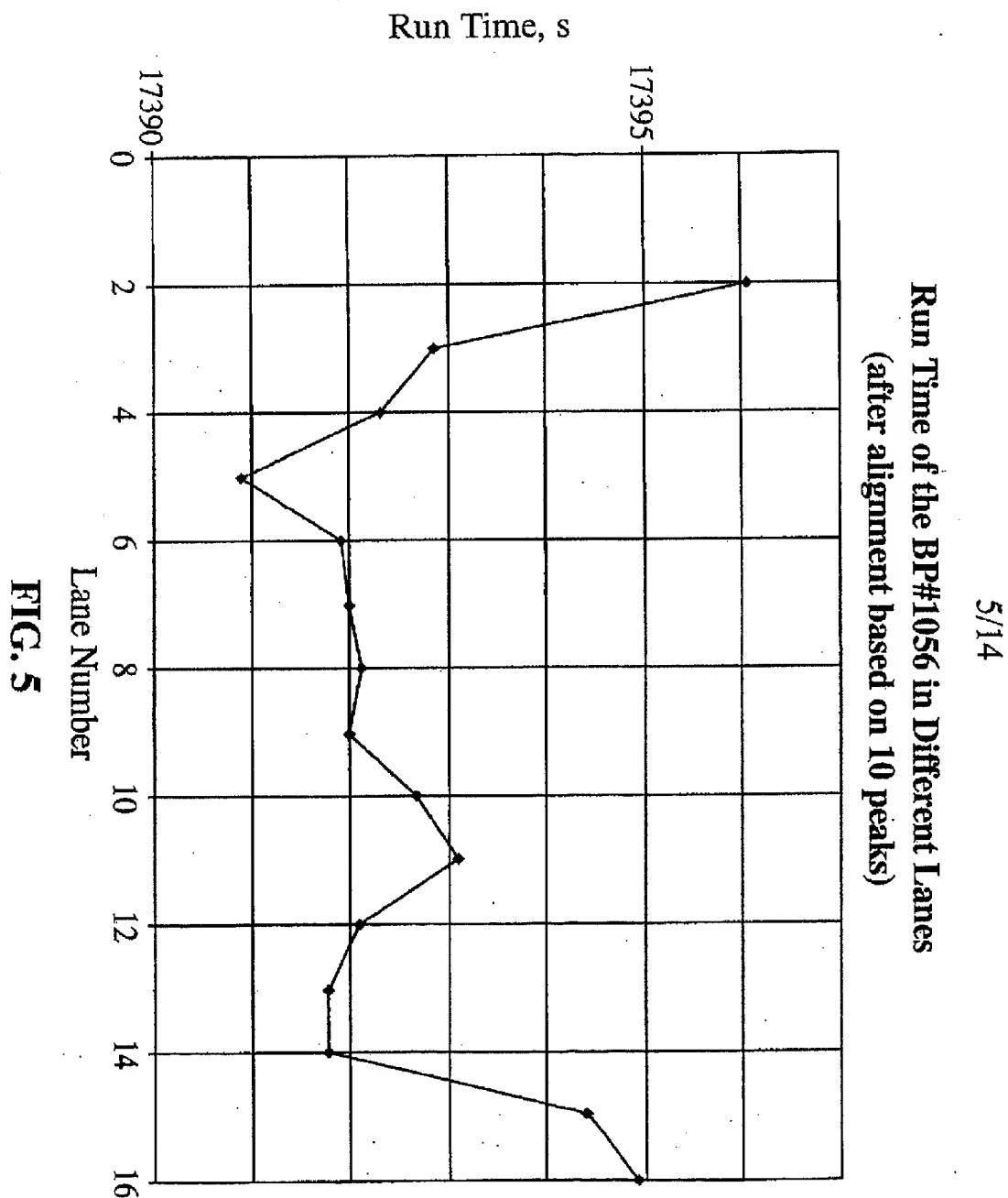
Standard Deviation (%) of the Spacing Between Adjacent Bases from  
Average as a Function of Number of Peaks Used as a Reference for  
Alignment of Raw Data

**FIG. 3**



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FIG. 4



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# HIV-1 TruGene Kit (version 0.80)

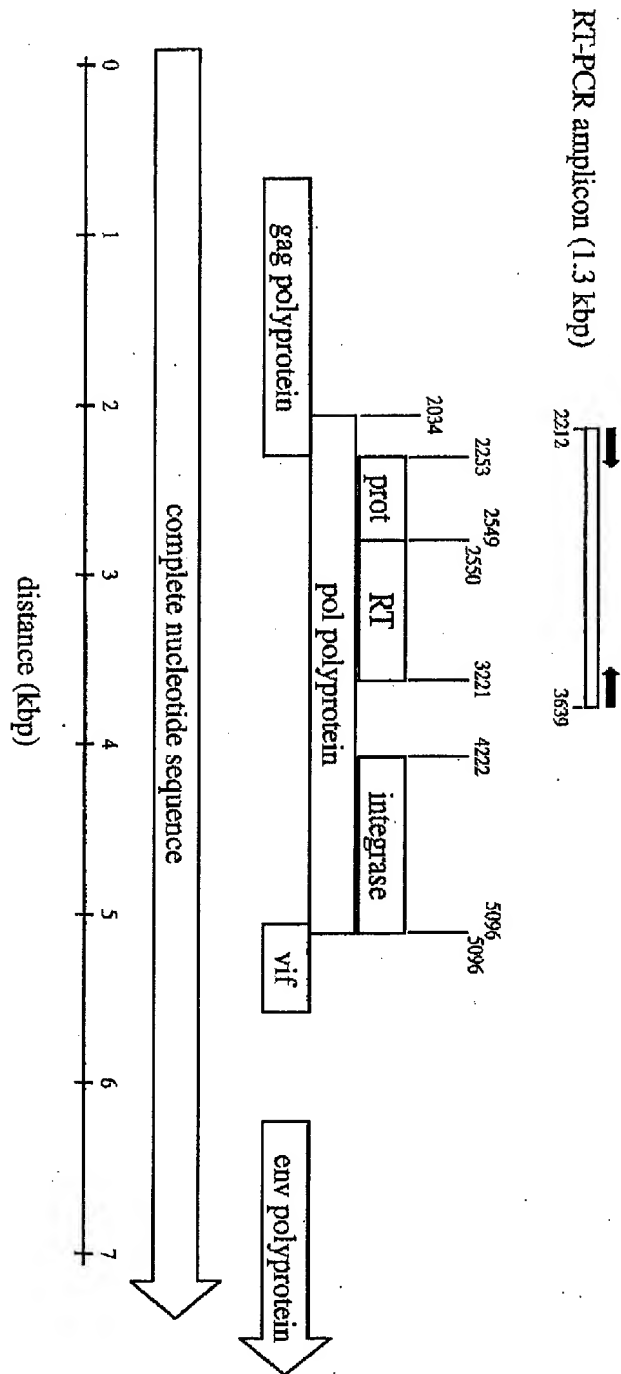


FIG. 6

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## Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

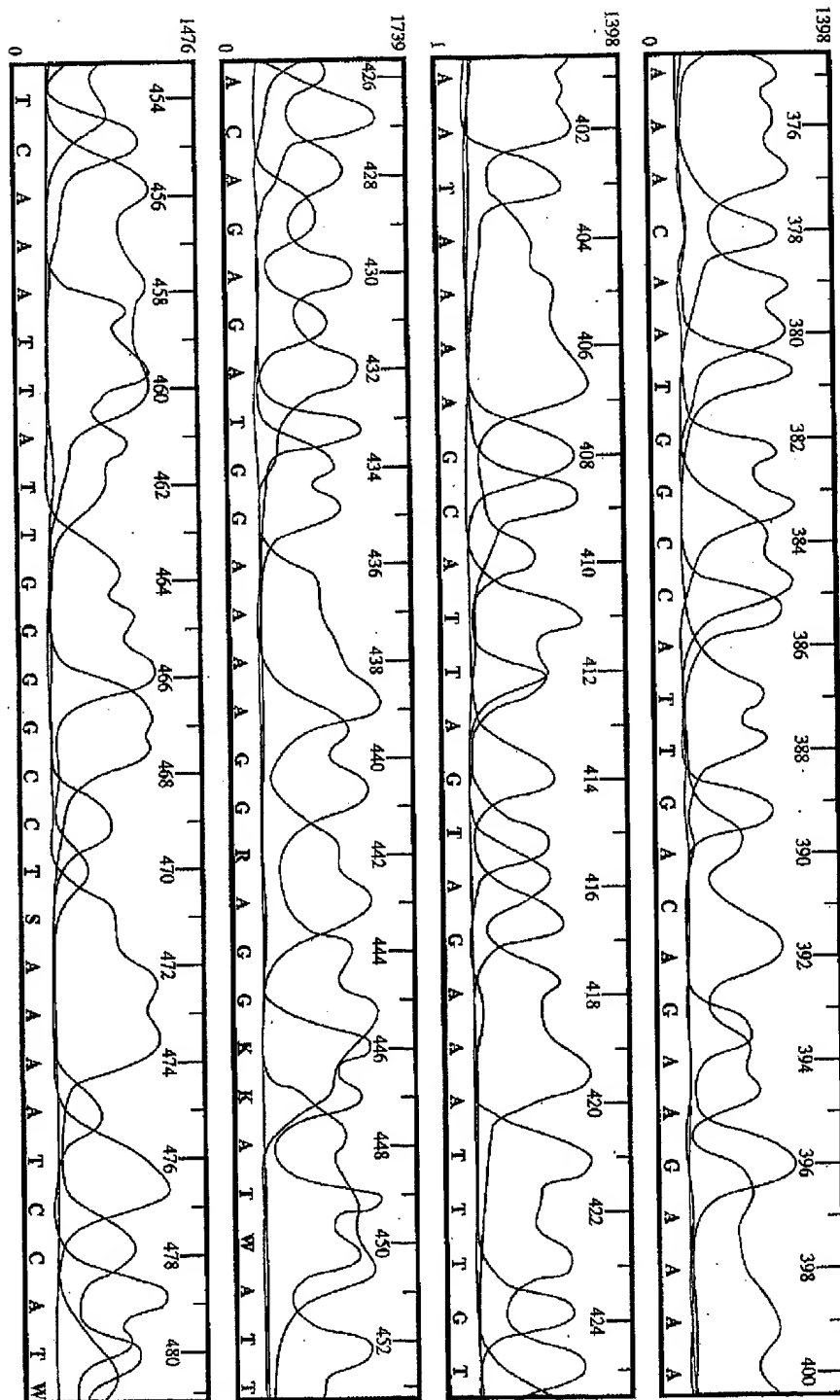


FIG. 7

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# Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

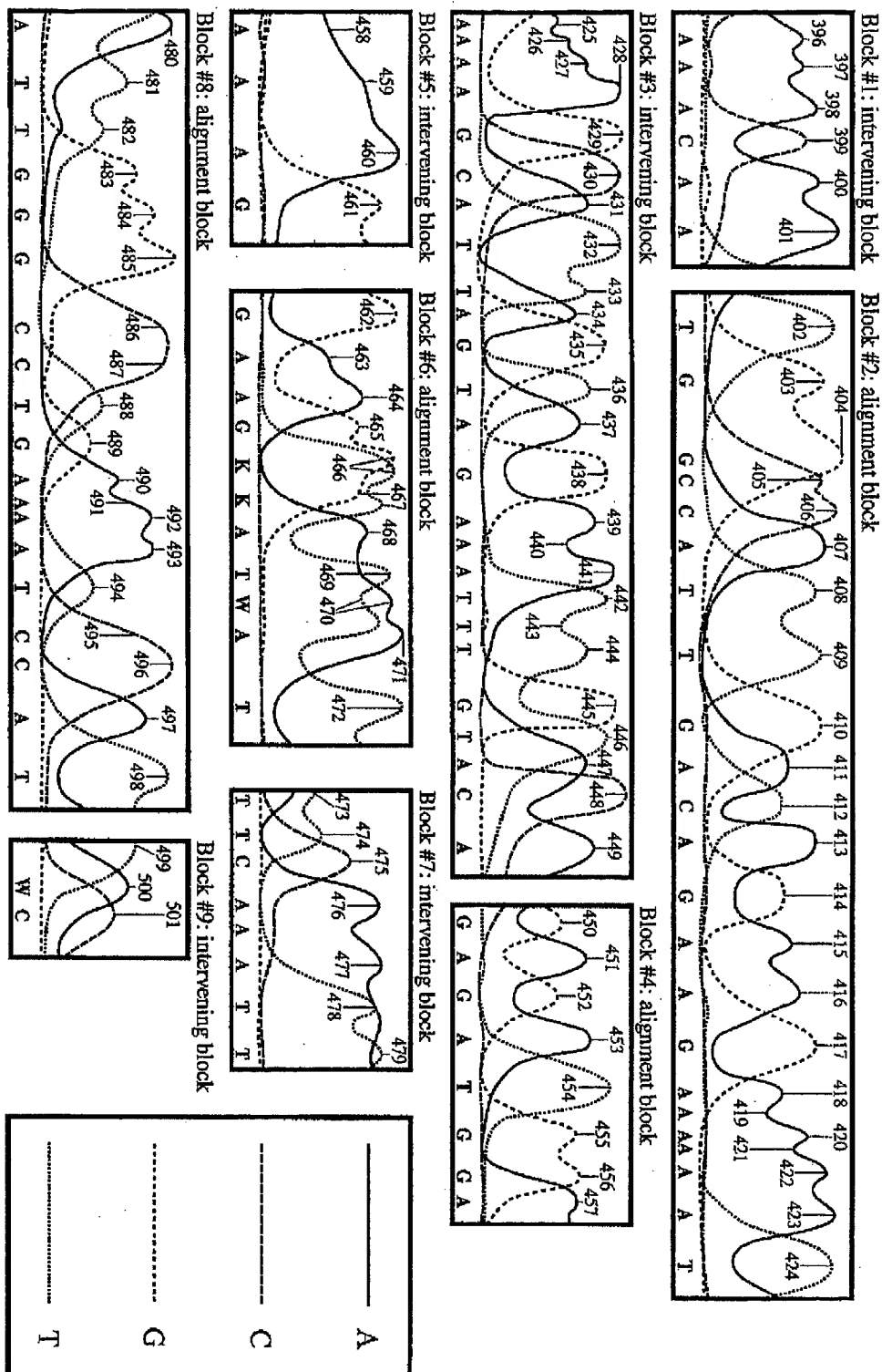


FIG. 8



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# Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

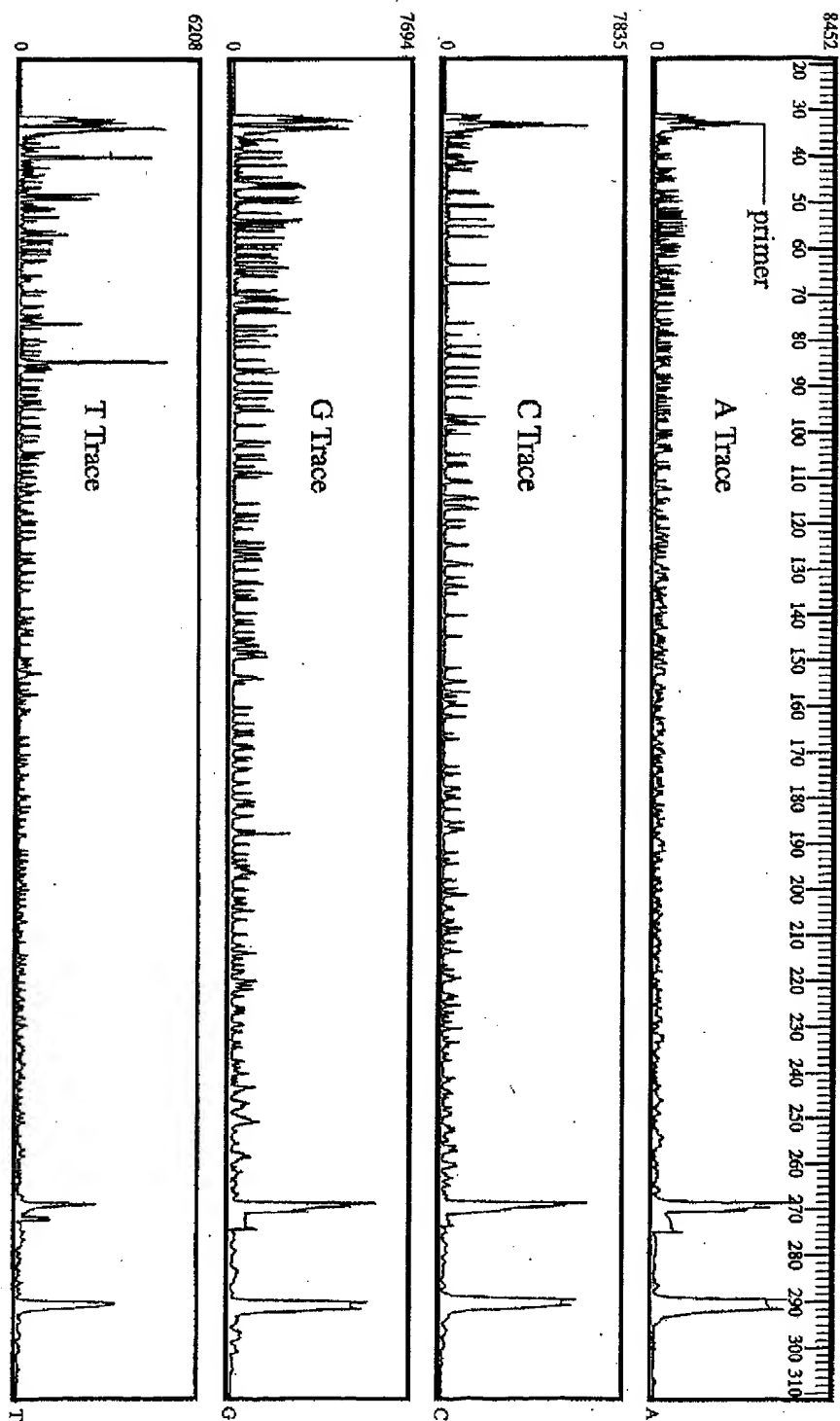


FIG. 9A

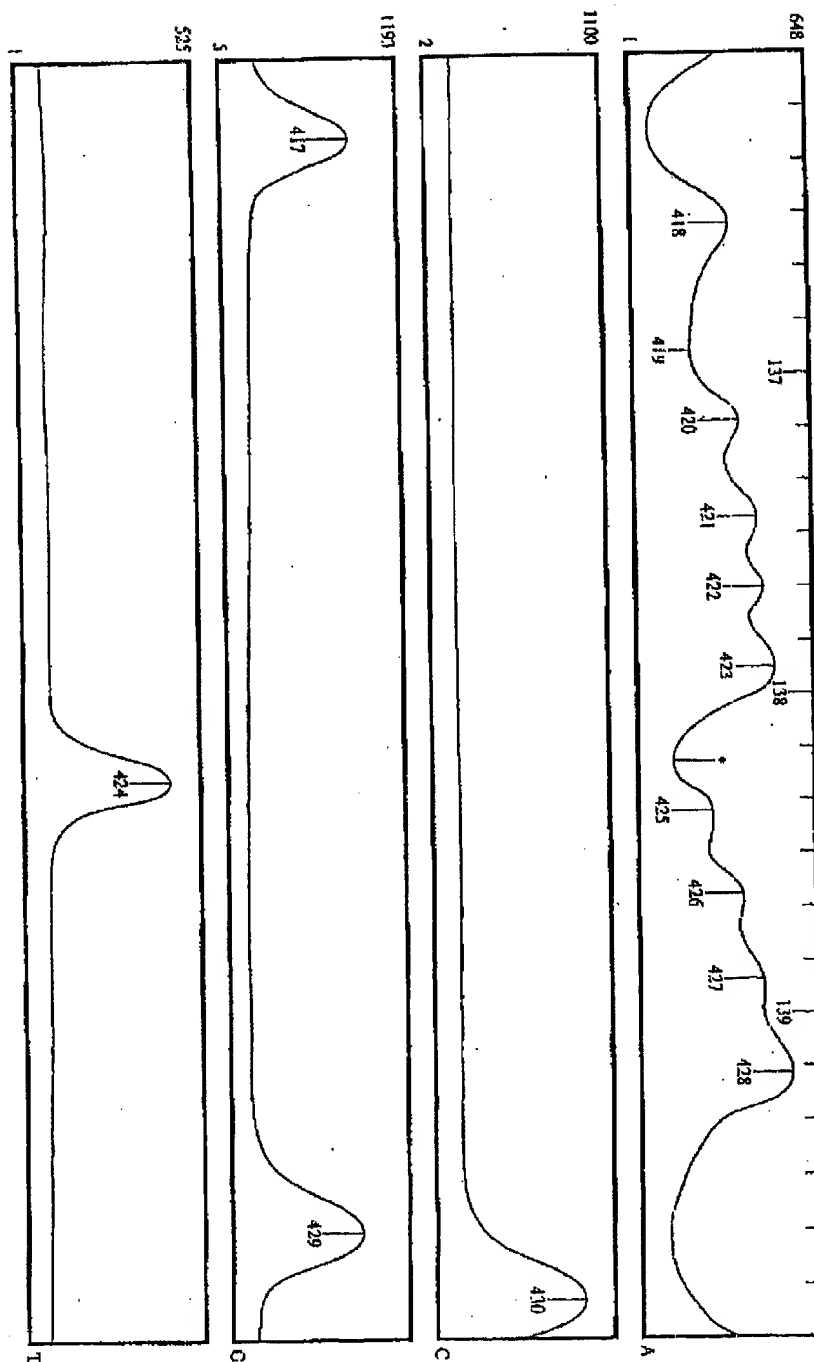
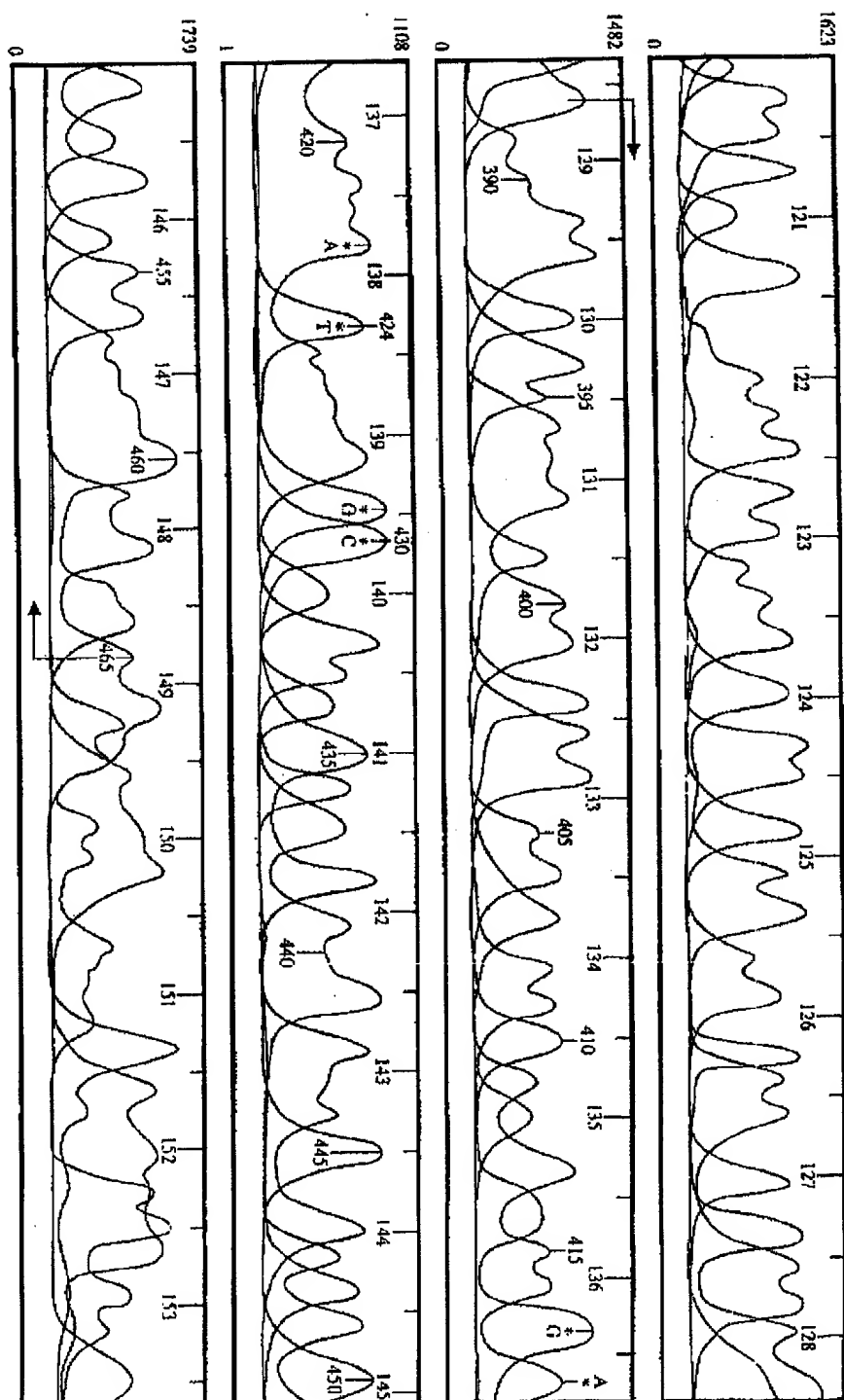


FIG. 9B

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**Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc****FIG. 9C**

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Deviation of the Peak Position (in Number of Bases) from the Average  
as a Function of Base Number in Different Traces Before Alignment

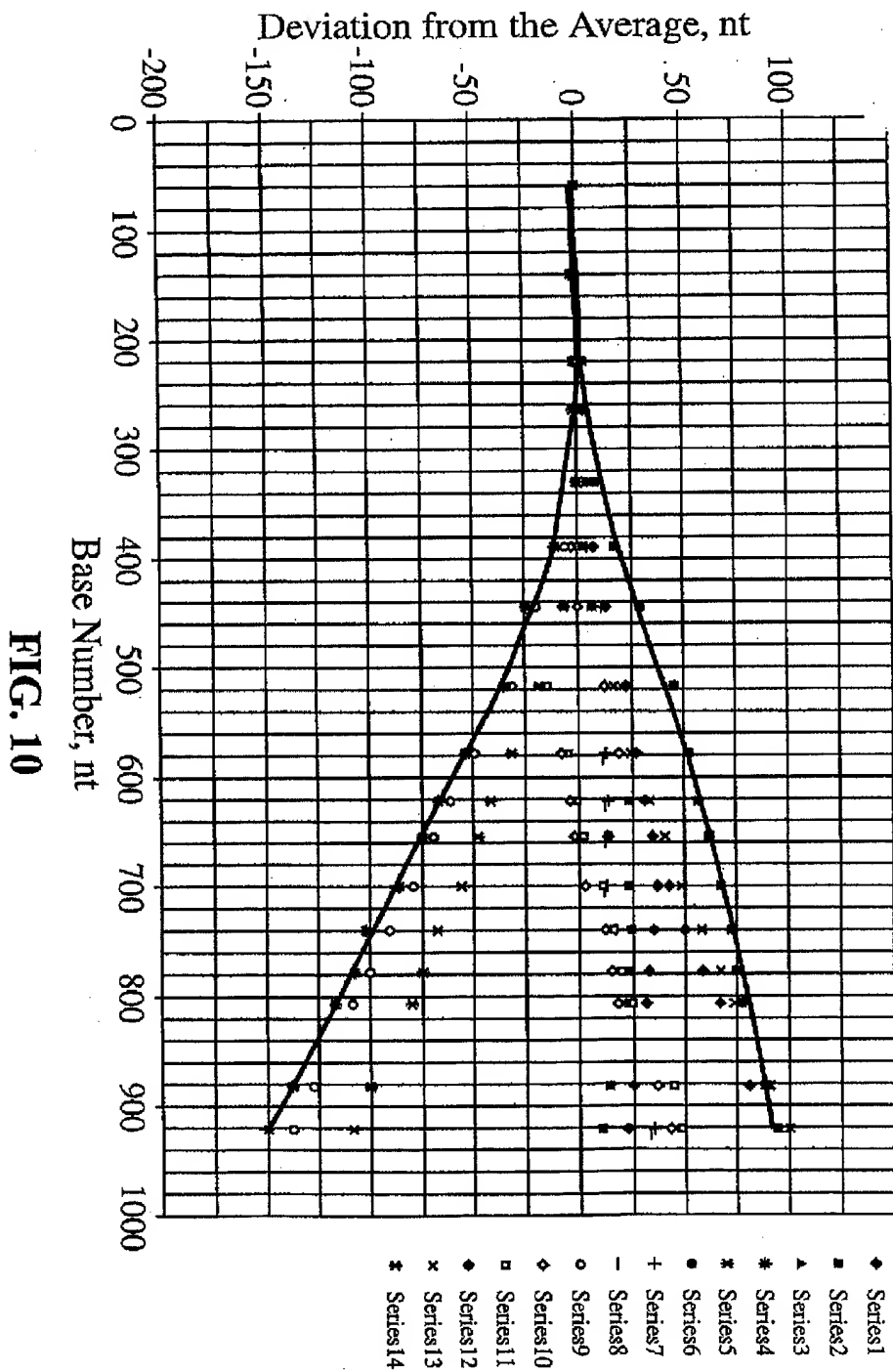


FIG. 10

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Deviation of the Peak Position (in Number of Bases) from the Average  
as a Function of Base Number in the Traces Aligned with Internal Standards  
(long gel, M13, 17 peaks, 5-th degree polynomial)

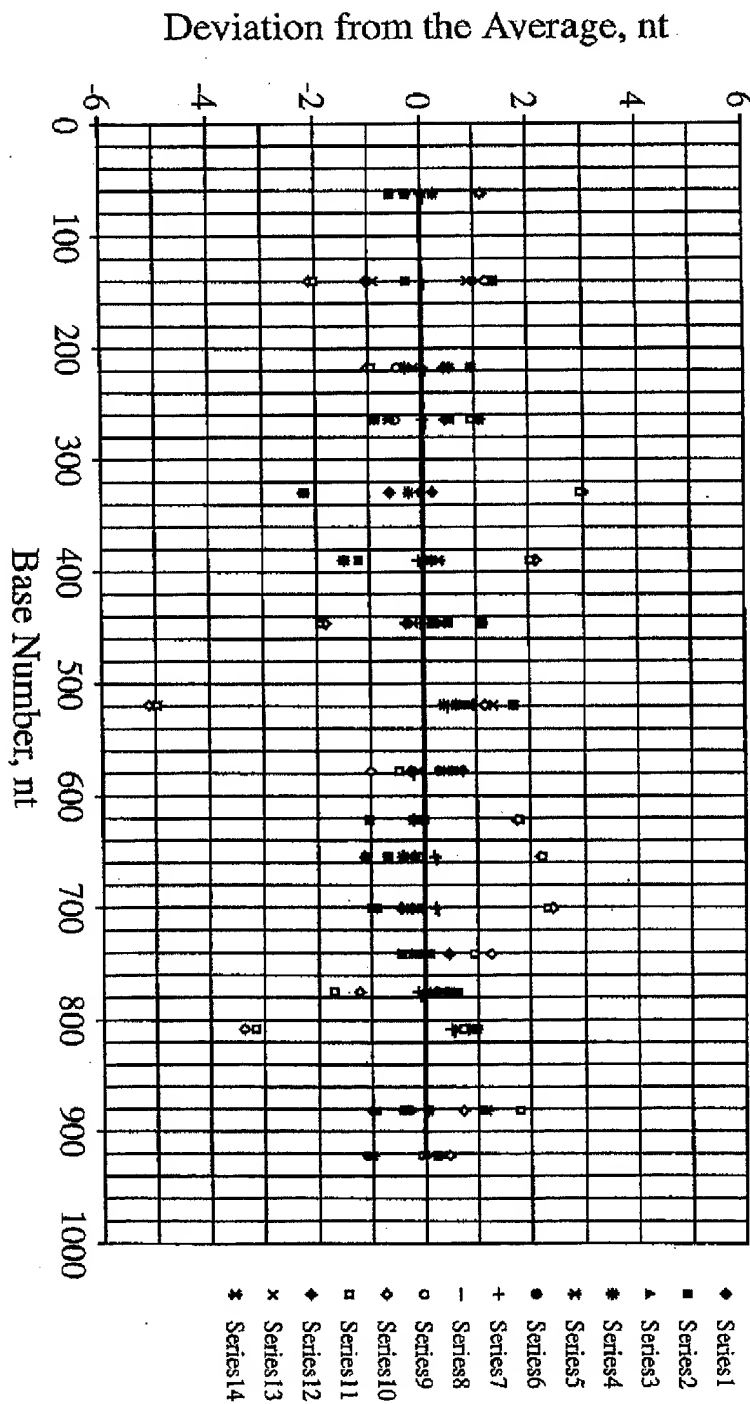


FIG. 11

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Deviation of the Peak Position from the Average as a Function  
of Base Number in the Traces Aligned with Internal Standards  
(Jong gel, M13, 6 peaks, 5-th degree polynomial)

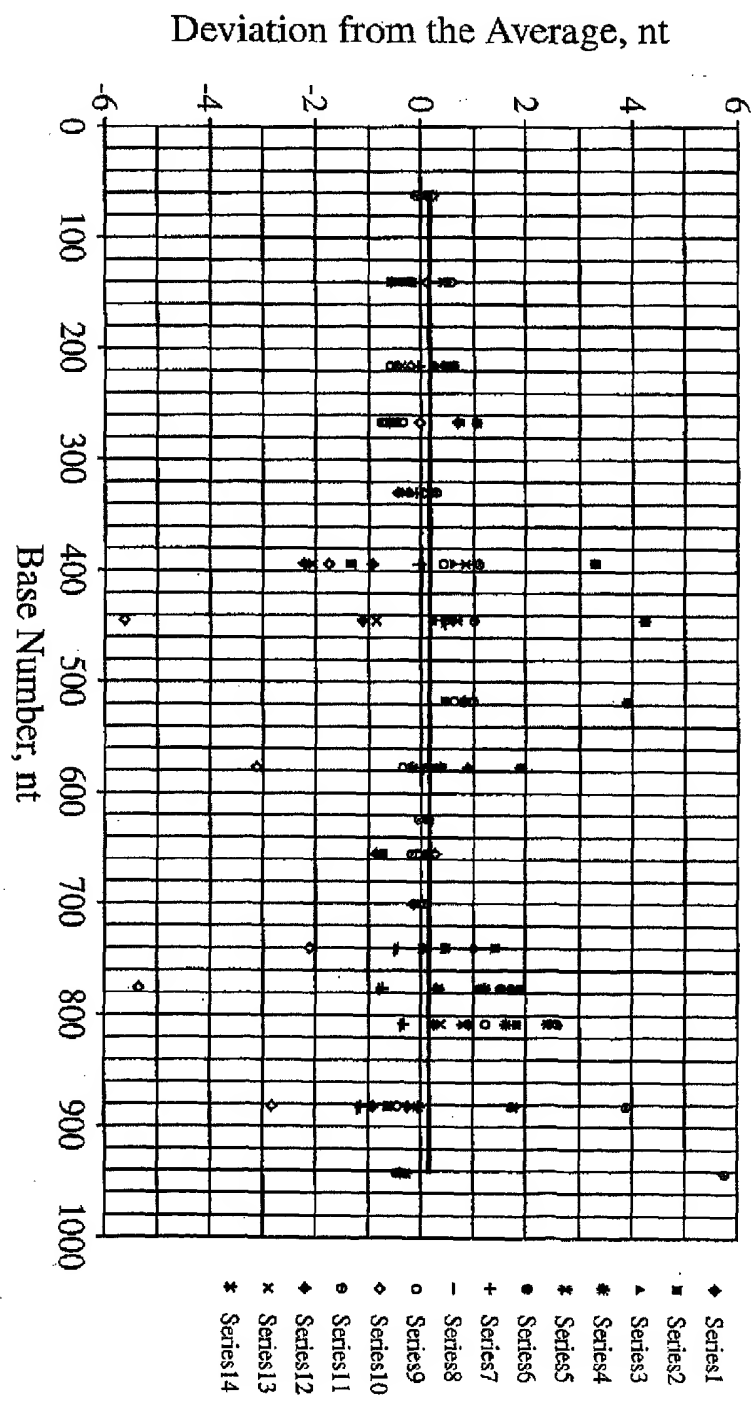


FIG. 12